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RAW SEQUENCE LISTING

DATE: 03/25/2002

PATENT APPLICATION: US/09/934,289A

TIME: 10:37:49

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\03252002\I934289A.raw

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6 <110> APPLICANT: Busfield, Samantha J.
8 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE
9   HERPESVIRUS-ENTRY-MEDIATOR-RELATED
10  PROTEIN FAMILY AND USES THEREOF
12 <130> FILE REFERENCE: MBIO98-061CP1CN1(M)
14 <140> CURRENT APPLICATION NUMBER: 09/934,289A
15 <141> CURRENT FILING DATE: 2001-08-21
17 <150> PRIOR APPLICATION NUMBER: US 09/342,767
18 <151> PRIOR FILING DATE: 1999-06-29
20 <150> PRIOR APPLICATION NUMBER: US 09/146,950
21 <151> PRIOR FILING DATE: 1998-09-03
23 <160> NUMBER OF SEQ ID NOS: 58
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1929
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (297)...(875)
36 <400> SEQUENCE: 1
37   gtcgacccac gcgtccgctc ggctttgcct ggacagctcc tgccctccgc agggcccacc      60
38   tgtgtccccc agcgccgctc caccagcag gcctgagccc ctctctgctg ccagacaccc      120
39   cctgtctgcc actctcctgc tgctcggtt ctgaggcaca gcttgtcaca ccgaggcgga      180
40   ttctctttct ctttctcttt ctctctggtc ccacagccgc agcaatggcg ctgagttcct      240
41   ctgctggagt tcctcctgct agctgggttc ccgagctgcc ggtctgagcc tgaggc atg      299
42                                     Met
43                                     1
45   gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga      347
46   Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg
47       5                      10                      15
49   acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc      395
50   Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro
51       20                      25                      30
53   tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg      443
54   Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val
55       35                      40                      45
57   ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag      491
58   Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu
59       50                      55                      60                      65
61   gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc      539
62   Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly
63       70                      75                      80

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65 acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa      587
66 Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln
67      85      90      95
69 atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg      635
70 Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg
71      100      105      110
73 aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc      683
74 Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val
75      115      120      125
77 cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc      731
78 Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser
79 130      135      140      145
81 ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc ctg      779
82 Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu
83      150      155      160
85 tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag      827
86 Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu
87      165      170      175
89 gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac ctc      875
90 Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu
91      180      185      190
93 tgaggtctca tcttgagct gccaccagcc cagcctccct gggacctgtc ttcactgcct      935
94 gggggccctgg gagccaggga ggctccctga ggctgagtga acactgggag ctgcacctgc      995
95 ctctcccacg tctcggccc cactcccga ggtgcagctg gctggtgacg aaggccggag      1055
96 ctgggaccag cagctcccac tgggtatggt ggtttctctc agggagcctc gtcacgtca      1115
97 ttgtttgctc cacagttggc ctaatcatat gtgtgaaaag aagaaagcca aggggtgatg      1175
98 tagtcaaggt gatcgtctcc atccagcggg aaagacagga ggcagaaggt gaggccacag      1235
99 tcattgaggc cctgcaggcc cctccggacg tcaccacggt ggccgtggag gagacaatac      1295
100 cctcattcac ggggaggagc ccaaaccact gaccacaga ctctgcaccc cgaagccaga      1355
101 gatacctgga gcgacggctg ctgaaagagg ctgtccacct ggcgaaacca ccggagcccg      1415
102 gaggttgagg ggctccgccc tgggtggct tccgtctcct ccagtggagg gagaggtggg      1475
103 gccctgctg gggtagagct ggggacgcca cgtgccatc ccatgggcca gtgagggcct      1535
104 ggggcctctg ttctgtgtg gcctgagctc cccagagtcc tgaggaggag cgcagttgc      1595
105 cctcgtctca cagaccacac acccagccct cctgggccag cccagagggc cctcagacc      1655
106 ccagctgtct gcgcgtctga ctcttggtggc ctcagcagga caggccccgg gcactgcctc      1715
107 acagccaagg ctggactggg ttggctgcag tgtggtgttt agtggatacc acatcggaag      1775
108 tgattttcta aattggattt gaattcggct cctgttttct atttgtcatg aaacagtgtg      1835
109 tttggggaga tgctgtggga ggatgtaaat atctgttttc tctcaaaaaa aaaaaaaaaa      1895
110 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa      1929
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 193
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <220> FEATURE:
118 <221> NAME/KEY: SIGNAL
119 <222> LOCATION: (1)...(38)
121 <400> SEQUENCE: 2
122 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
123      -35      -30      -25

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124 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
125      -20                      -15                      -10
126 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
127      -5                      1                      5                      10
128 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
129                      15                      20                      25
130 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
131                      30                      35                      40
132 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
133                      45                      50                      55
134 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
135                      60                      65                      70
136 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
137      75                      80                      85                      90
138 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
139                      95                      100                      105
140 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
141                      110                      115                      120
142 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
143                      125                      130                      135
144 Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp
145      140                      145                      150
146 Leu
147 155
149 <210> SEQ ID NO: 3
150 <211> LENGTH: 579
151 <212> TYPE: DNA
152 <213> ORGANISM: Homo sapiens
154 <220> FEATURE:
155 <221> NAME/KEY: CDS
156 <222> LOCATION: (1)...(579)
158 <400> SEQUENCE: 3
159 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc      48
160 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Trp Arg Ser Thr Pro
161 1      5      10      15
163 aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc      96
164 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
165      20      25      30
167 ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca      144
168 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
169      35      40      45
171. gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag      192
172 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
173      50      55      60
175 gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca      240
176 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
177      65      70      75      80
179 ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc      288
180 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys

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181                               85                               90                               95
183  caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc      336
184  Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
185                               100                               105                               110
187  agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc      384
188  Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
189                               115                               120                               125
191  gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc      432
192  Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
193                               130                               135                               140
195  agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc      480
196  Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
197  145                               150                               155                               160
199  ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg      528
200  Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
201                               165                               170                               175
203  gag gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac      576
204  Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp
205                               180                               185                               190
207  ctc                                                                    579
208  Leu
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 155
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 4
218  Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
219    1                               5                               10                               15
220  Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
221                               20                               25                               30
222  Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
223                               35                               40                               45
224  Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
225                               50                               55                               60
226  Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
227  65                               70                               75                               80
228  Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
229                               85                               90                               95
230  Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
231                               100                              105                              110
232  Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
233                               115                              120                              125
234  Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
235                               130                              135                              140
236  Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu
237  145                              150                              155
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 38
241 <212> TYPE: PRT

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242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: SIGNAL
246 <222> LOCATION: (1)...(38)
248 <400> SEQUENCE: 5
249 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
250      -35                      -30                      -25
251 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
252      -20                      -15                      -10
253 Pro Cys Tyr Ala Pro Ala
254      -5
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 114
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (1)...(114)
265 <400> SEQUENCE: 6
266 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc      48
267 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
268 1      5      10      15
270 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc      96
271 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
272      20      25      30
274 ccc tgc tac gcc cca gct      114
275 Pro Cys Tyr Ala Pro Ala
276      35
279 <210> SEQ ID NO: 7
280 <211> LENGTH: 34
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 7
285 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
286 1      5      10      15
287 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
288      20      25      30
289 Val Cys
292 <210> SEQ ID NO: 8
293 <211> LENGTH: 42
294 <212> TYPE: PRT
295 <213> ORGANISM: Homo sapiens
297 <400> SEQUENCE: 8
298 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
299 1      5      10      15
300 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
301      20      25      30
302 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
303      35      40

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VERIFICATION SUMMARY

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